

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/538, 291  
Source: JFWP  
Date Processed by STIC: 06/29/2006

***ENTERED***



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/538,291

DATE: 06/29/2006  
TIME: 13:48:04

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\06292006\J538291.raw

3 <110> APPLICANT: SHOWA DENKO K.K.  
W--> 4 <120> TITLE OF INVENTION: Method for screening E. coli strains which exhibit enhanced  
W--> 5 express of a foreign gene, such E. coli strains and method for  
W--> 6 producing protein or other compounds using the same  
W--> 7 <130> FILE REFERENCE: SDF4812PCT  
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/538,291  
C--> 8 <141> CURRENT FILING DATE: 2005-06-10  
8 <150> PRIOR APPLICATION NUMBER: JP 2002-360564  
9 <151> PRIOR FILING DATE: 2002-12-12  
W--> 10 <160> NUMBER OF SEQ ID: 2  
11 <170> SOFTWARE: PatentIn Ver. 2.1  
13 <210> SEQ ID NO: 1  
14 <211> LENGTH: 18  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Lithospermum erythrorhizon  
18 <400> SEQUENCE: 1  
19 taagcgtaat tagctgag 18  
21 <210> SEQ ID NO: 2  
22 <211> LENGTH: 18  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Lithospermum erythrorhizon  
26 <400> SEQUENCE: 2  
27 agatcgaaga tctaaaca 18

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/538,291

DATE: 06/29/2006

TIME: 13:48:05

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06292006\J538291.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:10 M:283 W: Missing Blank Line separator, <160> field identifier

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/538, 291

CRF Edit Date: 06/29/2006  
Edited by: DA

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

         Deleted:          invalid beginning/end-of-file text ;          page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

— Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

— Other:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

## **Raw Sequence Listing before editing (for reference only)**



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/538,291

DATE: 06/29/2006  
TIME: 10:21:32

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\06292006\J538291.raw

3 <110> APPLICANT: SHOWA DENKO K.K.  
W--> 4 <120> TITLE OF INVENTION: Method for screening *E. coli* strains which exhibit enhanced  
W--> 5 express of a foreign gene, such *E. coli* strains and method for  
W--> 6 producing protein or other compounds using the same  
W--> 7 <130> FILE REFERENCE: SDF4812PCT  
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/538,291  
C--> 8 <141> CURRENT FILING DATE: 2005-06-10  
8 <150> PRIOR APPLICATION NUMBER: JP 2002-360564  
9 <151> PRIOR FILING DATE: 2002-12-12  
W--> 10 <160> NUMBER OF SEQ ID: 2  
11 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
Corrected Diskette Needed

(pg-1)

## ERRORED SEQUENCES

21 <210> SEQ ID NO: 2  
22 <211> LENGTH: 18  
23 <212> TYPE: DNA  
24 <213> ORGANISM: *Lithospermum erythrorhizon*  
26 <400> SEQUENCE: 2  
27 agatcgaaga tctaaaca  
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E--> 36 1/2

18

deleted

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/538,291

DATE: 06/29/2006

TIME: 10:21:33

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06292006\J538291.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:10 M:283 W: Missing Blank Line separator, <160> field identifier  
L:34 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=2  
L:36 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:36 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:19 SEQ:2